

SEQUENCE LISTING

4110 - ZHANG, Hongyu et al.

4120 - ISOLATED HUMAN TRANSPORTER PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
AND USES THEREOF

4130 - CL001172

4160 - 4

4170 - FastSEQ for Windows Version 4.0

4210 - 1

4211 - 2195

4212 - DNA

4213 - Human

4400 - 1

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GenBank accession number: U001172.1. The sequence is a partial cDNA clone of the human gene for the protein p115, which is a member of the p115 family of proteins. The sequence is identical to the one reported in GenBank.

[illegible]

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(1) The sequence data were obtained from the GenBank database. The accession number for the sequence is U001172.

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(1) The sequence data were obtained from the GenBank database. The accession number for the sequence is CE001172.

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Sequence data from the following sources: GenBank, EMBL, DDBJ, and the International Nucleotide Sequence Database Collaboration (INSDC).

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Sequence data from GenBank accession number F01172.1. The sequence is a partial cDNA clone of a human gene. The sequence is 79740 bp long. The sequence is in the 5' to 3' direction. The sequence is in the forward orientation. The sequence is in the 5' to 3' direction. The sequence is in the forward orientation.



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GenBank accession number: U001172.1 (Chromosome I, 1,172,000 bp). The sequence is a partial clone of the chromosome I, 1,172,000 bp. The sequence is a partial clone of the chromosome I, 1,172,000 bp.

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(1) The sequence data were obtained from the GenBank database. The accession number is CL001172.

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The above sequence was obtained from the sequencing of the DNA of the *Escherichia coli* strain *W*3103. The sequence is identical to the sequence of the DNA of the *Escherichia coli* strain *W*3103.

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(1) The above sequence was determined by the method of Maxam and Gilbert (1980) using the Maxam-Gilbert sequencing kit (Pharmacia LKB, Beverly, MA).

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GenBank accession number: U001172.1 (Chromosome I, complete sequence).  
 Date of release: 1998-07-01. Version: 1.0.

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GenBank accession number: F01172.1. This sequence was submitted to GenBank on 10/10/91. The sequence is 192600 bp long.

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(1) The sequence data were obtained from the GenBank database. The accession number is CL001172.

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GenBank accession number: F01172.1. The sequence was determined by the Maxam-Gilbert method. The sequence is identical to the sequence in GenBank accession number F01172.1.

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The information on this page is derived from the GenBank database. The accession number for this sequence is CL001172. The sequence is a DNA sequence.



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Sequence of the DNA fragment (261420-264420) from the pUC19 vector. The sequence is presented in a 10-column format, with the first column containing the sequence number and the subsequent columns containing the sequence data. The sequence is presented in a 10-column format, with the first column containing the sequence number and the subsequent columns containing the sequence data.

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Sequence data from GenBank accession number U001172. The sequence is a DNA sequence, and the numbers on the right indicate the position of each line in the sequence.

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Sequence data from the following sources: GenBank, EMBL, DDBJ, and the International Nucleotide Sequence Database Collaboration (INSDC).

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GenBank accession number: U001172.1. The sequence was determined by the Sanger method. The sequence is identical to the sequence in GenBank.

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The above sequence was generated by the program "SeqGen" (version 1.0.0) using the parameters: "Random" (seed: 12345), "Length: 10000", "Alphabet: DNA", "GC Content: 50%", "Model: IUPAC", "Output: FASTA".





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Sequence data from GenBank accession number U001172. The sequence is a partial cDNA clone of the human gene for the protein p115, which is a member of the p115 family of proteins. The sequence is 349920 nucleotides long and is organized into 11 exons and 10 introns. The sequence is presented in a standard format with the first column containing the nucleotide sequence, the second column containing the corresponding amino acid sequence, and the third column containing the position of the sequence in the gene.

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GenBank accession number: U001172.1 (Chromosome I, 3,670,200 bp). The sequence is presented in 60 bp lines, with line numbers on the right.



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Thr Cys Asp Phe Leu His Gly Pro Glu Thr Lys Arg His Asp Ile Ala			
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Gln Ile Ala Gln Ala Leu Leu Gly Ser Glu Glu Arg Lys Val Glu Val			
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Ile Pro Val Lys Asn Gln Glu Gly Val Ala Met Met Phe Ile Ile Asn			
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Phe Glu Tyr Val Thr Asp Asn Glu Asn Ala Ala Thr Pro Glu Arg Val			
130	135	140	
Asn Pro Ile Leu Pro Ile Lys Thr Val Asn Arg Lys Phe Phe Gly Phe			
145	150	155	160
Lys Phe Pro Gly Leu Arg Val Leu Thr Tyr Arg Lys Gln Ser Leu Pro			
165	170	175	
Gln Glu Asp Pro Asp Val Val Val Ile Asp Ser Ser Lys His Ser Asp			
180	185	190	
Asp Ser Val Ala Met Lys His Phe Lys Ser Pro Thr Lys Glu Ser Cys			
195	200	205	
Ser Pro Ser Glu Ala Asp Asp Thr Lys Ala Leu Ile Gln Pro Ser Lys			
210	215	220	
Cys Ser Pro Leu Val Asn Ile Ser Gly Pro Leu Asp His Ser Ser Pro			
225	230	235	240
Lys Arg Gln Trp Asp Arg Leu Tyr Pro Asp Met Leu Gln Ser Ser Ser			
245	250	255	
Gln Leu Ser His Ser Arg Ser Arg Glu Ser Leu Cys Ser Ile Arg Arg			
260	265	270	
Ala Ser Ser Val His Asp Ile Glu Gly Phe Gly Val His Pro Lys Asn			
275	280	285	
Ile Phe Arg Asp Arg His Ala Ser Glu Asp Asn Gly Arg Asn Val Lys			
290	295	300	
Gly Pro Phe Asn His Ile Lys Ser Ser Leu Leu Gly Ser Thr Ser Asp			
305	310	315	320
Ser Asn Leu Asn Lys Tyr Ser Thr Ile Asn Lys Ile Pro Gln Leu Thr			
325	330	335	
Leu Asn Phe Ser Gln Val Lys Thr Ile Lys Lys Asn Ser Ser Pro Pro			
340	345	350	
Ser Ser Asp Lys Thr Ile Ile Ala Pro Lys Val Lys Asp Arg Thr His			
355	360	365	
Asn Val Thr Glu Lys Val Thr Gln Val Leu Ser Leu Gly Ala Asp Val			
370	375	380	
Leu Pro Glu Tyr Lys Leu Gln Thr Pro Arg Ile Asn Lys Phe Thr Ile			
385	390	395	400
Leu His Tyr Ser Pro Phe Lys Ala Val Trp Asp Trp Leu Ile Leu Leu			
405	410	415	

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Asp Ile Leu Ile Asn Ile Arg Thr Thr Tyr Val Asn Gln Asn Glu Glu  
465 470 475 480  
Val Val Ser Asp Pro Ala Lys Ile Ala Ile His Tyr Ile Lys Gly Trp  
485 490 495  
Phe Leu Ile Asp Met Val Ala Ala Ile Pro Phe Asp Leu Leu Ile Phe  
500 505 510  
Gly Ser Gly Ser Asp Glu Thr Thr Thr  
515 520